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GenCore version 5.1.3
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ON protein - nucleic search, using frame_plus_p2n model

Run on: November 9, 2002, 07:39:20 ; Search time 69 seconds
(without alignments)
844.472 Million cell updates/sec

Title: US-09-895-298A-83

Perfect score: 190

Sequence: 1 MNFFQPPSKAWRASQMMTFF.....HDGSDLRLRSRRSVOEGNPR A 190

Scoring table: OLIGO

Xgapext 60.0 , Xgapext 60.0
Ygapext 60.0 , Ygapext 60.0
Fgapext 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 441362 seqs, 153338381 residues

Word size: 4

Total number of hits satisfying chosen parameters: 161137

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Command line parameters:

```
-MODEL=frame_plus_model -DEV=x1p
-Q=/cgn2_1/USP10_spool/US09895298/runat_06112002_160753_3595/app_query.fasta_1_327
-DB=issued_Patents_NA -QFM=fastap -SFIX=oaligna.rni -MINMATCH=6.1 -LOOPCI=0
-LOOPEXT=0 -UNITS=bts -SPART=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=4 -ALIGN=15 -MODE=LOCAL
-OUTFM=pto -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09895298 @CGN 1_31 @runat_06112002_160753_3595 -NCPU=6 -ICPU=3
-NO_XLPIX -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV -TIMEOUT=120
-WARN_TIMEOUT=30 -THRESHOLD=1 -XGAPEXT=60 -XGAPPOP=60 -FGAPPOP=6 -FGAPEXT=7
-YGAPPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7
```

Database : Issued_Patents_NA:*

```
1: /cgn2_6/prodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/prodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCITS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfile1.seq:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	8	4.2	592	4 US-09-328-111-39
2	8	4.2	1825	4 US-09-184-964-1
3	7	3.7	56	2 US-08-244-434-6
4	7	3.7	56	2 US-08-244-434-6
5	7	3.7	237	4 US-09-134-001C-1756
6	7	3.7	257	1 US-08-700-575-4
7	7	3.7	320	4 US-09-183-266A-18
8	7	3.7	336	2 US-09-577-492-36
9	7	3.7	336	4 US-09-799-620-36
10	7	3.7	387	1 US-09-329-884-1
11	7	3.7	418	4 US-09-221-017B-915
12	7	3.7	525	4 US-09-329-884-15

RESULT 1
US-09-328-111-39
Sequence 39, Application US/09328111
; Sequence 39, Application US/09328111
; Patent No. 626333

GENERAL INFORMATION:

APPLICANT: Endege, Wilson O.
APPLICANT: Steinmann, Kathleen E.
APPLICANT: Astle, Jon H.
APPLICANT: Burgess, Christopher C.
APPLICANT: Bushnell, Steven E.
APPLICANT: Carroll III, Eddie
APPLICANT: Catino, Theodore J.
APPLICANT: Dertli, Adnan
APPLICANT: Ford, Donna M.
APPLICANT: Lewis, Marcia E.
APPLICANT: Monahan, John E.
APPLICANT: Schliegel, Robert

TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS

FILE REFERENCE: CCD-257 (US)

CURRENT APPLICATION NUMBER: US/09/328,111

CURRENT FILING DATE: 1999-06-08

EARLIER APPLICATION NUMBER: US 60/088,801

EARLIER FILING DATE: 1998-06-10

NUMBER OF SEQ ID NOS: 850

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 39

LENGTH: 592

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE: misc-feature

NAME/KEY: misc-feature

LOCATION: (1) .(592)

OTHER INFORMATION: n = A,T,C or G

US-09-328-111-39

Query Match: 3.68% Indels: 0
 DB: 1 Gaps: 0

US-09-895-298a-83 (1-190) x US-08-700-575-4 (1-257)

QY 50 GIPYPropheArgGlyLeuPro 56
 DB 234 GGACCTTTCAGGGGACTCCA 214

RESULT 7
 US-09-183-266A-18/C
 Sequence 18, Application US/09183266A
 Patent No. 6361954

GENERAL INFORMATION:
 APPLICANT: Stillman, Bruce
 APPLICANT: Williams, R. Sanders
 APPLICANT: Mendez, Juan
 TITLE OF INVENTION: DNA REPLICATION-REGULATING GENES
 FILE REFERENCE: CSHL9-01A3
 CURRENT FILING DATE: 1998-10-30
 PRIOR APPLICATION NUMBER: PCT/US97/07333
 PRIOR FILING DATE: 1997-05-02
 PRIOR APPLICATION NUMBER: 08/648,650
 PRIOR FILING DATE: 1996-05-15
 PRIOR APPLICATION NUMBER: 08/643,034
 NUMBER OF SEQ ID NOS: 50
 SOFTWARE: Fast-SEQ for Windows Version 3.0
 SEQ ID NO 18
 LENGTH: 320
 TYPE: DNA
 ORGANISM: H. sapiens
 US-09-183-266A-18

Alignment Scores:
 pred. No.: 95.3
 Score: 7.00
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 3.68%
 DB: 4
 Gaps: 0

Length: 320
 Matches: 7
 Conservative: 0
 Mismatches: 0
 Indels: 0

US-09-895-298a-83 (1-190) x US-09-183-266A-18 (1-320)

QY 21 IlePheLeuLeuPhePhePro 27
 DB 133 ATCTTCCGTCCTCTTCCTTCCC 113

RESULT 8
 US-08-577-492-36

QY 36 Application US/08577492

GENERAL INFORMATION:
 APPLICANT: Owens, Raymond John
 APPLICANT: Perry, Martin John
 APPLICANT: Lumb, Simon Mark
 TITLE OF INVENTION: HUMAN PHOSPHODESTERASE TYPE IVC, AND
 TITLE OF INVENTION: ITS PRODUCTION AND USE
 NUMBER OF SEQUENCES: 40
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & NO. 6291197-15
 STREET: One Liberty Place, 46th floor
 CITY: Philadelphia
 STATE: PA
 COUNTRY: USA
 ZIP: 19103

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS DOS
 SOFTWARE: Wordperfect 6.1

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US 08/577,492
 FILING DATE:
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: GB 9426227.6
 FILING DATE: 23-DEC-1994
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: GB 9512996.1
 FILING DATE: 26-JUN-1995

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US 08/577,492
 FILING DATE: 22-DEC-1995
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: GB 9426227.6
 FILING DATE: 23-DEC-1994
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: GB 9512996.1
 FILING DATE: 26-JUN-1995

REGISTRATION NUMBER: 35.099
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (215) 568-3100
 TELEFAX: (215) 568-3439
 INFORMATION FOR SEQ ID NO: 36:
 SEQENCE CHARACTERISTICS:
 LENGTH: 336 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear

US-08-577-492-36

Alignment Scores:
 pred. No.: 100
 Score: 7.00
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 3.68%
 DB: 2
 Gaps: 0

Length: 336
 Matches: 7
 Conservative: 0
 Mismatches: 0
 Indels: 0

US-09-895-298a-83 (1-190) x US-08-577-492-36 (1-336)

QY 178 ArgSerArgGargSerValGln 184
 DB 21 CGCAGTCGGCGTCGGTCCAG 41

RESULT 9
 US-09-079-630-36

QY 36 Application US/09079630

GENERAL INFORMATION:
 APPLICANT: Owens, Raymond John
 APPLICANT: Perry, Martin John
 APPLICANT: Lumb, Simon Mark
 TITLE OF INVENTION: HUMAN PHOSPHODESTERASE TYPE IVC, AND
 TITLE OF INVENTION: ITS PRODUCTION AND USE
 NUMBER OF SEQUENCES: 40
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & NO. 6291197-15
 STREET: One Liberty Place, 46th floor
 CITY: Philadelphia
 STATE: PA
 COUNTRY: USA
 ZIP: 19103

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS DOS
 SOFTWARE: Wordperfect 6.1

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US 08/577,492
 FILING DATE:
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: GB 9426227.6
 FILING DATE: 23-DEC-1994
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: GB 9512996.1
 FILING DATE: 26-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Cherry, David A.

REGISTRATION NUMBER: 35,099

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568-3100

TELEFAX: (215) 568-3439

INFORMATION FOR SEQ ID NO: 36:

SEQUENCE CHARACTERISTICS:

LENGTH: 336 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

US-09-079-630-36

Alignment Scores:

Pred. No.: 100

Score: 7.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 3.68%

DB: 4

Gaps: 0

US-09-895-298a-83 (1-190) x US-09-079-630-36 (1-336)

Qy 178 ArgSerArgArgSerValGln 184

Db 21 CGCAGTGGCGCTCGGTCCAG 41

RESULT 10

US-09-329-884-1

Sequence 1, application US/09329884

PATENT NO. 6342233

GENERAL INFORMATION:

APPLICANT: Irvin, Randall T.

TITLE OF INVENTION: PSUDOMONAS TREATMENT

TITLE OF INVENTION: COMPOSITION AND METHOD

FILE REFERENCE: 8900-0008.30

CURRENT APPLICATION NUMBER: US/09/329,884

CURRENT FILING DATE: 1999-06-11

EARLIER APPLICATION NUMBER: US 60/089,155

EARLIER FILING DATE: 1998-06-12

NUMBER OF SEQ ID NOS: 22

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO: 1

LENGTH: 387

TYPE: DNA

FEATURE: Pseudomonas aeruginosa

NAME/KEY: CDS

LOCATION: (0)...(0)

US-09-329-884-1

Alignment Scores:

Pred. No.: 115

Score: 7.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 3.68%

DB: 4

Gaps: 0

US-09-895-298a-83 (1-190) x US-09-329-884-1 (1-387)

Qy 163 GlngGlypheleuhisIeugly 169

Db 300 CAAGGTTCTTCACATTTGGGC 320

RESULT 11

US-09-221-017B-915/C

; Sequence 915, Application US/09221017B

; Patent No. 6444799

; GENERAL INFORMATION:

; APPLICANT: Ross, Bruce C.

TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF

NAME: Monroy, Gladys H

NUMBER OF SEQUENCES: 1120

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FOERSTER

STREET: 755 PAGE MILL ROAD

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304-1018

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows

SOFTWARE: FASTSEQ for Windows Version 2.0b

CURRENt APPLICATION DATA:

APPLICATION NUMBER: US/09/221,017B

CLASSIFICATION:

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: PP1182

FILING DATE: 31-DEC-1997

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: PP1546

FILING DATE: 09-APR-1998

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: PCT/AU98/01023

FILING DATE: 10-DEC-1998

ATTORNEY/AGENT INFORMATION:

NAME: Monroy, Gladys H

REGISTRATION NUMBER: 32,430

REFERENCE/DOCKET NUMBER: 21340-20021.00

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-813-5500

TELEX: 706141

INFORMATION FOR SEQ ID NO: 915:

SEQUENCE CHARACTERISTICS:

TELEFAX: 650-494-0792

TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

LENGTH: 418 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

LENGTH: 418 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

LENGTH: 418 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

LENGTH: 418 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

LENGTH: 418 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

LENGTH: 418 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

LENGTH: 418 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

LENGTH: 418 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

LENGTH: 418 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

LENGTH: 418 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

LENGTH: 418 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

LENGTH: 418 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

LENGTH: 418 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

LENGTH: 418 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

LENGTH: 418 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

LENGTH: 418 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

LENGTH: 418 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

LENGTH: 418 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

LENGTH: 418 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

LENGTH: 418 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

LENGTH: 418 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

LENGTH: 418 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

LENGTH: 418 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

LENGTH: 418 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

LENGTH: 418 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

LENGTH: 418 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

LENGTH: 418 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

LENGTH: 418 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

LENGTH: 418 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

LENGTH: 418 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

LENGTH: 418 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

LENGTH: 418 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

LENGTH: 418 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

LENGTH: 418 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

LENGTH: 418 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

LENGTH: 418 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

LENGTH: 418 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

RESULT 14
US-09-140-235-26/C
US-09-140-235-26/C
Sequence 26, Application US/09740235
Patent No. 644041
GENERAL INFORMATION:
APPLICANT: Krasnow, Randie E.
APPLICANT: Warren, Bridget A.
APPLICANT: Baugh, Mariah R.
TITLE OF INVENTION: COLON CANCER MARKER
FILE REFERENCE: PC-0031 CIP
CURRENT APPLICATION NUMBER: US/09/740,235
CURRENT FILING DATE: 2000-12-18
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PERL Program
SEQ ID NO 36
LENGTH: 567
TYPE: DNA
ORGANISM: Rattus norvegicus
FEATURE: misc-feature
NAME/KEY: Incyte ID No. 6448041 702081830HL
OTHER INFORMATION: Incyte ID No. 6448041 702081830HL
US-09-740-235-26
Alignment Scores:
Pred. No.: 168 Length: 567
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.68% Indels: 0
DB: 4 Gaps: 0
QY 163 GlnglyPheLeuIleLeuGly 169
DB 438 CAGGGTCTTACACTGGC 458

RESULT 13
US-09-329-884-17
Sequence 17, Application US/09329884
Patient No. 634233
GENERAL INFORMATION:
APPLICANT: Irvin, Randall T.
APPLICANT: Hodges, Robert S.
TITLE OF INVENTION: PSEUDOMONAS TREATMENT
FILE REFERENCE: 8900-0008_30
CURRENT APPLICATION NUMBER: US/09/329, 884
CURRENT FILING DATE: 1999-06-11
EARLIER APPLICATION NUMBER: US 60/089, 155
EARLIER FILING DATE: 1998-06-12
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 17
LENGTH: 525
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
FEATURE: CDS
NAME/KEY: CDS
LOCATION: (0)...(0)
US-09-329-884-17

Alignment Scores:
Pred. No.: 156 Length: 525
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.68% Indels: 0
DB: 4 Gaps: 0
QY 163 GlnglyPheLeuIleLeuGly 169
DB 438 CAGGGTCTTACACTGGC 458

RESULT 15
PCT-US91-01691-27/C
Sequence 27, Application PC/US9201691
GENERAL INFORMATION:
APPLICANT: LIVAK, KENNETH J.
APPLICANT: RAFALSKI, J. A.
APPLICANT: SHEPHERD, NANCY S.
TITLE OF INVENTION: METHOD OF IDENTIFYING A
TITLE OF INVENTION: NUCLEOTIDE PRESENT AT A
TITLE OF INVENTION: DEFINED POSITION IN A
TITLE OF INVENTION: NUCLEIC ACID
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: DU PONT COMPANY
STREET: BARLEY MILL PLAZA 36/2152
CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: USA
ZIP: 19800-0036
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh System, 6.0
SOFTWARE: Microsoft Word, 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/01691
FILING DATE: 19920312
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/669, 568
FILING DATE: March 13, 1991
ATTORNEY/AGENT INFORMATION:
NAME: GALLEGO, R. THOMAS
REFERENCE/DOCKET NUMBER: CR-8918
TELECOMMUNICATION INFORMATION:

TELEPHONE: 302-892-7342
TELEFAX: 302-892-7949
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 603 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
PCT-US92-01691-27

Alignment Scores:

Prd. No.:	179	Length:	603
Score:	7.00	Matches:	7
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	3.68%	Indels:	0
DB:	5	Gaps:	0

US-09-895-298A-83 (1-190) x PCT-US92-01691-27 (1-603)

Qy 23 LeuleuphepheProSerphe 29
||| ||||| ||||| ||||| |||||
Db 247 CTACATTTTCCATCTTC 227

Search completed: November 9, 2002, 09:10:04
Job time : 72 secs

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